CMA_all_case_studies

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First, read in all of the source data

```
source("~/Desktop/CH3_impacts_meta_analysis/scripts/ch_3_raw_data.R")
```

Then, load all the packages we need

```
library(tinytex)
library(dplyr)
library(ggplot2)
library(ggthemes)
library(metaviz)
library(metafor)
```

Calculate effect sizes for each study in the database

```
effect_sizes_richness <- escalc("ROM", # effect size for the meta analysis (e.g., RD, RR, OR, SMD)
                                m1i = raw_data_imputed$mean_invaded,
                                n1i = raw_data_imputed$sample_size_invaded, # Then, follow with all of
                                sd1i = raw_data_imputed$SD_invaded,
                                m2i = raw_data_imputed$mean_control,
                                n2i = raw_data_imputed$sample_size_control,
                                sd2i = raw_data_imputed$SD_control,
                                data = raw_data_imputed)
```

Look through the first few effect sizes

```
head(effect_sizes_richness)
```

Run a cumulative meta-analysis for all of the data

Order the studies by year

```
ordered_by_year <- arrange(effect_sizes_richness, publicationyear)
head(ordered_by_year)
dim(ordered_by_year)
```

Run the random effects model using all data

```
random_effects_model_ordered <- rma(yi=ordered_by_year$yi,
                            vi=ordered_by_year$vi,
                            method = "REML",
                            test = "knha",
                            data=ordered_by_year)
random_effects_model_ordered
```

```
##
## Random-Effects Model (k = 334; tau^2 estimator: REML)
##
## tau^2 (estimated amount of total heterogeneity): 0.1923 (SE = 0.0179)
## tau (square root of estimated tau^2 value):      0.4385
## I^2 (total heterogeneity / total variability):   96.07%
```

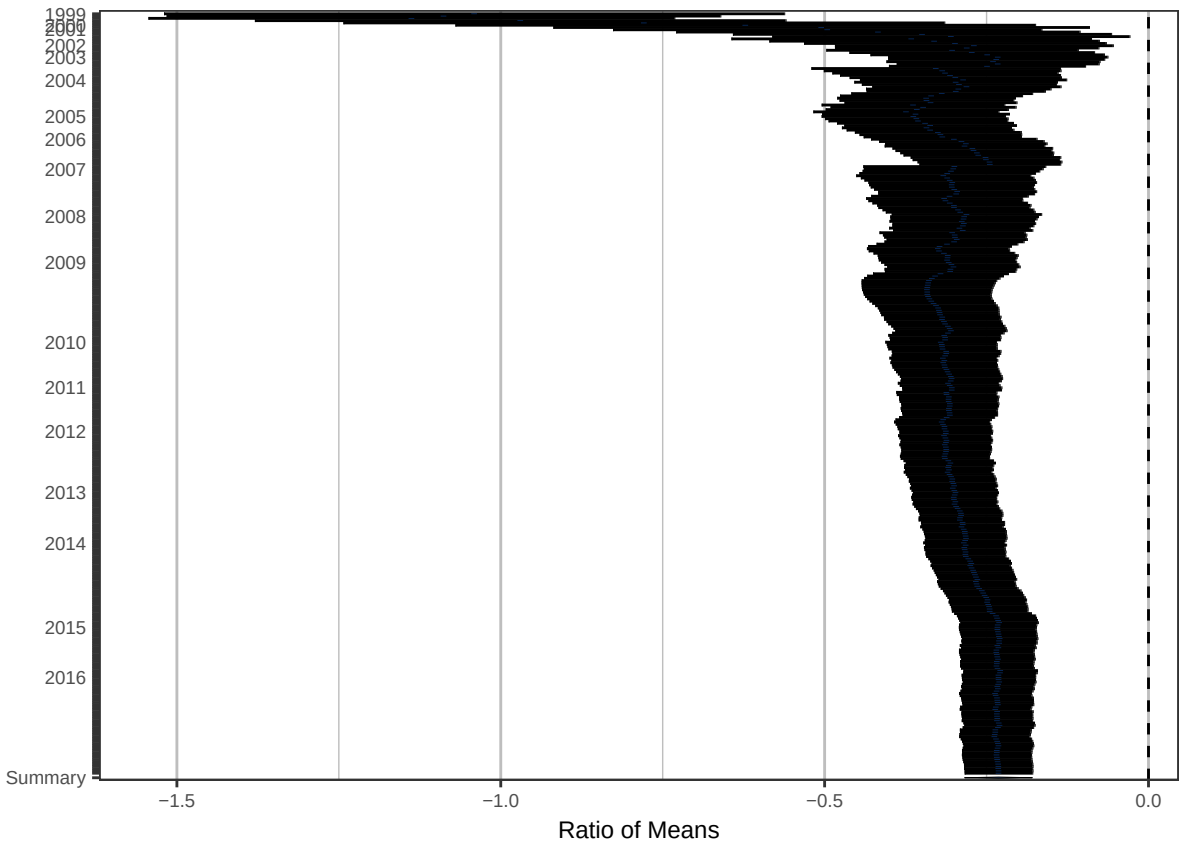
```
## H^2 (total variability / sampling variability):  25.43
##
## Test for Heterogeneity:
## Q(df = 333) = 3303.4327, p-val < .0001
##
## Model Results:
##
## estimate      se     tval    pval    ci.lb    ci.ub
##  -0.2316  0.0286  -8.0898  <.0001  -0.2879  -0.1753  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Create study labels for the CMA plots

```
plyr::count(ordered_by_year$publicationyear)
overall_CMA_study_labels <- c(1999,
                              strrep("", 1:4),
                              2000,
                              strrep("",1),
                              2001,
                              strrep("",1:6),
                              2002,
                              strrep("",1:4),
                              2003,
                              strrep("",1:9),
                              2004,
                              strrep("",1:15),
                              2005,
                              strrep("",1:9),
                              2006,
                              strrep("",1:12),
                              2007,
                              strrep("",1:20),
                              2008,
                              strrep("",1:19),
                              2009,
                              strrep("",1:34),
                              2010,
                              strrep("",1:19),
                              2011,
                              strrep("",1:18),
                              2012,
                              strrep("",1:26),
                              2013,
                              strrep("",1:21),
                              2014,
                              strrep("",1:36),
                              2015,
                              strrep("",1:21),
                              2016,
                              strrep("",1:42))
```

Make the overall cumulative meta-analysis

```
forest_plot_CMA <- viz_forest(
  x = random_effects_model_ordered,
  method = "REML",
  #study_labels = ordered_by_year[1:334, "code"], # include study name label
  study_labels = overall_CMA_study_labels, # include custom study labels that skip any   repeated years
  xlab = "Ratio of Means", # make a label along x-axis for effect size
  col = "Blues",
  type = "cumulative",
  text_size = 3)
forest_plot_CMA
```



Print the file to a PDF

```
pdf(file="~/Desktop/CH3_impacts_meta_analysis/figures/CMA_all_case_studies.pdf")
forest_plot_CMA
dev.off()
```

```
## pdf
##   2
```

```
dev.off()
```

```
## null device
##           1
```

If we want to summarize the data from the first five studies, we can use this code

```
forest_plot_CMA$data
first_five_effect <- c(-1.04112114,-1.0883960,-1.1379484,-0.9699270,-0.7790654)
```

```
first_five_low_ci <- c(-1.5198541,-1.5157978,-1.5438819,-1.3795680,-1.2429049)
first_five_high_ci <- c(-0.56238815,-0.66099414,-0.73201492,-0.56028606,-0.31522604)
mean(first_five_effect)
exp(-1.003292)
1-0.3666704 # this is richness decline
mean(first_five_low_ci)
mean(first_five_high_ci)

-1.003292 - 1.440401
-1.003292 + 0.5661819
```